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RAW SEQUENCE LISTING DATE: 09/30/2002
 PATENT APPLICATION: US/10/055,797 TIME: 08:10:34

Input Set : N:\Crf3\Datashold\EFS\10055797\GNCA-P03-007SequenceListing.txt
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3 <110> APPLICANT: Hammond et al.
 5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE
 7 <130> FILE REFERENCE: GNCA-P03-007
 9 <140> CURRENT APPLICATION NUMBER: 10/055,797
 10 <141> CURRENT FILING DATE: 2002-01-22
 12 <150> PRIOR APPLICATION NUMBER: 60/189,739
 W--> 13 <151> PRIOR FILING DATE: PCT/US01/08435
 15 <160> NUMBER OF SEQ ID NOS: 17
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 5775
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(5775)
 27 <223> OTHER INFORMATION:
 29 <400> SEQUENCE: 1
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 31 Met Lys Ser Pro Ala Leu Gln Pro Leu Ser Met Ala Gly Leu Gln Leu
 32 1 5 10 15
 33 atg acc cct gct tcc tca cca atg ggt cct ttc ttt gga ctg cca tgg 96
 34 Met Thr Pro Ala Ser Ser Pro Met Gly Pro Phe Phe Gly Leu Pro Trp
 35 20 25 30
 36 caa caa gaa gca att cat gat aac att tat acg cca aga aaa tat cag 144
 37 Gln Gln Glu Ala Ile His Asp Asn Ile Tyr Thr Pro Arg Lys Tyr Gln
 38 35 40 45
 39 gtt gaa ctg ctt gaa gca gct ctg gat cat aat acc atc gtc tgt tta 192
 40 Val Glu Leu Leu Glu Ala Ala Leu Asp His Asn Thr Ile Val Cys Leu
 41 50 55 60
 42 aac act ggc tca ggg aag aca ttt att gct agt act act cta cta aag 240
 43 Asn Thr Gly Ser Gly Lys Thr Phe Ile Ala Ser Thr Thr Leu Leu Lys
 44 65 70 75 80
 45 agc tgt ctc tat cta gat cta ggg gag act tca gct aga aat gga aaa 288
 46 Ser Cys Leu Tyr Leu Asp Leu Gly Glu Thr Ser Ala Arg Asn Gly Lys
 47 85 90 95
 48 agg acg gtg ttc ttg gtc aac tct gca aac cag gtt gct caa caa gtg 336
 49 Arg Thr Val Phe Leu Val Asn Ser Ala Asn Gln Val Ala Gln Gln Val
 50 100 105 110
 51 tca gct gtc aga act cat tca gat ctc aag gtt ggg gaa tac tca aac 384
 52 Ser Ala Val Arg Thr His Ser Asp Leu Lys Val Gly Glu Tyr Ser Asn
 53 115 120 125
 54 cta gaa gta aat gca tct tgg aca aaa gag aga tgg aac caa gag ttt 432

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55	Leu	Glu	Val	Asn	Ala	Ser	Trp	Thr	Lys	Glu	Arg	Trp	Asn	Gln	Glu	Phe	
56	130						135					140					
57	act	aag	cac	cag	gtt	ctc	att	atg	act	tgc	tat	gtc	gcc	ttg	aat	gtt	480
58	Thr	Lys	His	Gln	Val	Leu	Ile	Met	Thr	Cys	Tyr	Val	Ala	Leu	Asn	Val	
59	145						150					155				160	
60	ttg	aaa	aat	ggt	tac	tta	tca	ctg	tca	gac	att	aac	ctt	ttg	gtg	ttt	528
61	Leu	Lys	Asn	Gly	Tyr	Leu	Ser	Leu	Ser	Asp	Ile	Asn	Leu	Leu	Val	Phe	
62							165				170				175		
63	gat	gag	tgt	cat	ctt	gca	atc	cta	gac	cac	ccc	tat	cga	gaa	ttt	atg	576
64	Asp	Glu	Cys	His	Ile	Ala	Ile	Leu	Asp	His	Pro	Tyr	Arg	Glu	Phe	Met	
65							180				185				190		
66	aag	ctc	tgt	gaa	att	tgt	cca	tca	tgt	cct	cgc	att	ttg	gga	cta	act	624
67	Lys	Leu	Cys	Glu	Ile	Cys	Pro	Ser	Cys	Pro	Arg	Ile	Leu	Gly	Leu	Thr	
68							195				200				205		
69	gct	tcc	att	tta	aat	ggg	aaa	tgg	gat	cca	gag	gat	ttg	gaa	gaa	aag	672
70	Ala	Ser	Ile	Leu	Asn	Gly	Lys	Trp	Asp	Pro	Glu	Asp	Leu	Glu	Glu	Lys	
71							210				215				220		
72	ttt	cag	aaa	cta	gag	aaa	att	ctt	aag	agt	aat	gct	gaa	act	gca	act	720
73	Phe	Gln	Lys	Leu	Glu	Lys	Ile	Leu	Lys	Ser	Asn	Ala	Glu	Thr	Ala	Thr	
74							225				230				235	240	
75	gac	ctg	gtg	gtc	tta	gac	agg	tat	act	tct	cag	cca	tgt	gag	att	gtg	768
76	Asp	Leu	Val	Val	Leu	Asp	Arg	Tyr	Thr	Ser	Gln	Pro	Cys	Glu	Ile	Val	
77							245				250				255		
78	gtg	gat	tgt	gga	cca	ttt	act	gac	aga	agt	ggg	ctt	tat	gaa	aga	ctg	816
79	Val	Asp	Cys	Gly	Pro	Phe	Thr	Asp	Arg	Ser	Gly	Leu	Tyr	Glu	Arg	Leu	
80							260				265				270		
81	ctg	atg	gaa	tta	gaa	gaa	gca	ctt	aat	ttt	atc	aat	gat	tgt	aat	ata	864
82	Leu	Met	Glu	Leu	Glu	Ala	Leu	Asn	Phe	Ile	Asn	Asp	Cys	Asn	Ile		
83							275				280				285		
84	tct	gta	cat	tca	aaa	gaa	aga	gat	tct	act	tta	att	tcg	aaa	cag	ata	912
85	Ser	Val	His	Ser	Lys	Glu	Arg	Asp	Ser	Thr	Leu	Ile	Ser	Lys	Gln	Ile	
86							290				295				300		
87	cta	tca	gac	tgt	cgt	gcc	gta	ttg	gta	gtt	ctg	gga	ccc	tgg	tgt	gca	960
88	Leu	Ser	Asp	Cys	Arg	Ala	Val	Leu	Val	Val	Leu	Gly	Pro	Trp	Cys	Ala	
89							305				310				315	320	
90	gat	aaa	gta	gct	gga	atg	atg	gta	aga	gaa	cta	cag	aaa	tac	atc	aaa	1008
91	Asp	Lys	Val	Ala	Gly	Met	Met	Val	Arg	Glu	Leu	Gln	Lys	Tyr	Ile	Lys	
92							325				330				335		
93	cat	gag	caa	gag	gag	ctg	cac	agg	aaa	ttt	tta	ttg	ttt	aca	gac	act	1056
94	His	Glu	Gln	Glu	Glu	Leu	His	Arg	Lys	Phe	Leu	Leu	Phe	Thr	Asp	Thr	
95							340				345				350		
96	ttc	cta	agg	aaa	ata	cat	gca	cta	tgt	gaa	gag	cac	ttc	tca	cct	gcc	1104
97	Phe	Leu	Arg	Lys	Ile	His	Ala	Leu	Cys	Glu	Glu	His	Phe	Ser	Pro	Ala	
98							355				360				365		
99	tca	ctt	gac	ctg	aaa	ttt	gta	act	cct	aaa	gta	atc	aaa	ctg	ctc	gaa	1152
100	Ser	Leu	Asp	Leu	Lys	Phe	Val	Thr	Pro	Lys	Val	Ile	Lys	Leu	Leu	Glu	
101							370				375				380		
102	atc	tta	cgc	aaa	tat	aaa	cca	tat	gag	cga	cac	agt	ttt	gaa	agc	gtt	1200
103	Ile	Leu	Arg	Lys	Tyr	Lys	Pro	Tyr	Glu	Arg	His	Ser	Phe	Glu	Ser	Val	

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104	385	390	395	400	
105	gag	tgg	tat	aat	1248
106	Glu	Trp	Tyr	Asn	
107	Asn	Arg	Asn	Gln	
108	Asp	Asp	Asp	Asp	
109	Ser	Glu	Asp	Asp	
110	Asp	Asp	Glu	Glu	
111	Asp	Phe	Pro	Ser	
112	Glu	Thr	Asn	Phe	
113	Asn	Asn	Pro	Phe	
114	Asp	Asp	Asp	Asp	
115	Phe	Val	Glu	Arg	
116	Arg	Arg	Tyr	Thr	
117	Tyr	Ala	Val	Ala	
118	Asn	Gly	Glu	Glu	
119	Asp	Lys	Gln	Glu	
120	Pro	Pro	Asp	Leu	
121	Glu	Ala	Gly	Ala	
122	Phe	Gly	His	Tyr	
123	Arg	Ile	Gly	Ile	
124	Lys	Gly	Ile	Gly	
125	Asn	Asn	Gly	Ile	
126	Gln	Pro	Arg	Asn	
127	Pro	Arg	Asn	Asn	
128	Arg	Asn	Asn	Asn	
129	Asp	Ile	Pro	Lys	
130	Pro	Ile	Lys	Cys	
131	Lys	Cys	Asn	Asn	
132	Asn	Ile	Pro	Lys	
133	Pro	Ile	Ile	Asn	
134	Ile	Asn	Asn	Asn	
135	Asn	Ile	Asn	Asn	
136	Tyr	Ile	Asn	Asn	
137	Ile	Asn	Asn	Asn	
138	Asp	Ile	Asn	Asn	
139	Leu	Asn	Asn	Asn	
140	Lys	Asn	Asn	Asn	
141	Asp	Ile	Asn	Asn	
142	Asp	Ile	Asn	Asn	
143	Asp	Ile	Asn	Asn	
144	Asp	Ile	Asn	Asn	
145	Asp	Ile	Asn	Asn	
146	Asp	Ile	Asn	Asn	
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148	Asp	Ile	Asn	Asn	
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154 Thr Arg Glu Leu Pro Asp Gly Thr Phe Tyr Ser Thr Leu Tyr Leu Pro	
155 . 660 665 670	
156 att aac tca cct ctt cga gcc tcc att gtt ggt cca cca atg agc tgt	2064
157 Ile Asn Ser Pro Leu Arg Ala Ser Ile Val Gly Pro Pro Met Ser Cys	
158 . 675 680 685	
159 gta cga ttg gct gaa aga gtt gtc gct ctc att tgc tgt gag aaa ctg	2112
160 Val Arg Leu Ala Glu Arg Val Val Ala Leu Ile Cys Cys Glu Lys Leu	
161 . 690 695 700	
162 cac aaa att ggc gaa ctg gat gac cat ttg atg cca gtt ggg aaa gag	2160
163 His Lys Ile Gly Glu Leu Asp Asp His Leu Met Pro Val Gly Lys Glu	
164 705 710 715 720	
165 act gtt aaa tat gaa gag gag ctt gat ttg cat gat gaa gaa gag acc	2208
166 Thr Val Lys Tyr Glu Glu Leu Asp Leu His Asp Glu Glu Glu Thr	
167 . 725 730 735	
168 agt gtt cca gga aga cca ggt tcc acg aaa cga agg cag tgc tac cca	2256
169 Ser Val Pro Gly Arg Pro Gly Ser Thr Lys Arg Arg Gln Cys Tyr Pro	
170 . 740 745 750	
171 aaa gca att cca gag tgt ttg agg gat agt tat ccc aga cct gat cag	2304
172 Lys Ala Ile Pro Glu Cys Leu Arg Asp Ser Tyr Pro Arg Pro Asp Gln	
173 . 755 760 765	
174 ccc tgt tac ctg tat gtg ata gga atg gtt tta act aca cct tta cct	2352
175 Pro Cys Tyr Leu Tyr Val Ile Gly Met Val Leu Thr Thr Pro Leu Pro	
176 . 770 775 780	
177 gat gaa ctc aac ttt aga agg cgg aag ctc tat cct cct gaa gat acc	2400
178 Asp Glu Leu Asn Phe Arg Arg Arg Lys Leu Tyr Pro Pro Glu Asp Thr	
179 785 790 795 800	
180 aca aga tgc ttt gga ata ctg acg gcc aaa ccc ata cct cag att cca	2448
181 Thr Arg Cys Phe Gly Ile Leu Thr Ala Lys Pro Ile Pro Gln Ile Pro	
182 . 805 810 815	
183 cac ttt cct gtg tac aca cgc tct gga gag gtt acc ata tcc att gag	2496
184 His Phe Pro Val Tyr Thr Arg Ser Gly Glu Val Thr Ile Ser Ile Glu	
185 . 820 825 830	
186 ttg aag aag tct ggt ttc atg ttg tct cta caa atg ctt gag ttg att	2544
187 Leu Lys Lys Ser Gly Phe Met Leu Ser Leu Gln Met Leu Glu Leu Ile	
188 . 835 840 845	
189 aca aga ctt cac cag tat ata ttc tca cat att ctt cgg ctt gaa aaa	2592
190 Thr Arg Leu His Gln Tyr Ile Phe Ser His Ile Leu Arg Leu Glu Lys	
191 . 850 855 860	
192 cct gca cta gaa ttt aaa cct aca gac gct gat tca gca tac tgt gtt	2640
193 Pro Ala Leu Glu Phe Lys Pro Thr Asp Ala Asp Ser Ala Tyr Cys Val	
194 865 870 875 880	
195 cta cct ctt aat gtt gtt aat gac tcc agc act ttg gat att gac ttt	2688
196 Leu Pro Leu Asn Val Val Asn Asp Ser Ser Thr Leu Asp Ile Asp Phe	
197 . 885 890 895	
198 aaa ttc atg gaa gat att gag aag tct gaa gct cgc ata ggc att ccc	2736
199 Lys Phe Met Glu Asp Ile Glu Lys Ser Glu Ala Arg Ile Gly Ile Pro	
200 . 900 905 910	
201 agt aca aag tat aca aaa gaa aca ccc ttt gtt ttt aaa tta gaa gat	2784

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203			915			920			925								
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205	Tyr	Gln	Asp	Ala	Val	Ile	Ile	Pro	Arg	Tyr	Arg	Asn	Phe	Asp	Gln	Pro	
206		930				935			940								
207	cat	cga	ttt	tat	gta	gct	gat	gtg	tac	act	gat	ctt	acc	cca	ctc	agt	2880
208	His	Arg	Phe	Tyr	Val	Ala	Asp	Val	Tyr	Thr	Asp	Leu	Thr	Pro	Leu	Ser	
209	945			950			955			960							
210	aaa	ttt	cct	tcc	cct	gag	tat	gaa	act	ttt	gca	gaa	tat	tat	aaa	aca	2928
211	Lys	Phe	Pro	Ser	Pro	Glu	Tyr	Glu	Thr	Phe	Ala	Glu	Tyr	Tyr	Lys	Thr	
212		965			970			975									
213	aag	tac	aac	ctt	gac	cta	acc	aat	ctc	aac	cag	cca	ctg	ctg	gat	gtg	2976
214	Lys	Tyr	Asn	Leu	Asp	Leu	Thr	Asn	Leu	Asn	Gln	Pro	Leu	Leu	Asp	Val	
215		980			985			990									
216	gac	cac	aca	tct	tca	aga	ctt	aat	ctt	ttg	aca	cct	cga	cat	ttg	aat	3024
217	Asp	His	Thr	Ser	Ser	Arg	Leu	Asn	Leu	Leu	Thr	Pro	Arg	His	Leu	Asn	
218		995			1000			1005									
219	cag	aag	ggg	aaa	gcg	ctt	cct	tta	agc	agt	gct	gag	aag	agg	aaa		3069
220	Gln	Lys	Gly	Lys	Ala	Leu	Pro	Leu	Ser	Ser	Ala	Glu	Lys	Arg	Lys		
221		1010				1015				1020							
222	gcc	aaa	tgg	gaa	agt	ctg	cag	aat	aaa	cag	ata	ctg	gtt	cca	gaa		3114
223	Ala	Lys	Trp	Glu	Ser	Leu	Gln	Asn	Lys	Gln	Ile	Leu	Val	Pro	Glu		
224		1025				1030			1035								
225	ctc	tgt	gct	ata	cat	cca	att	cca	gca	tca	ctg	tgg	aga	aaa	gct		3159
226	Leu	Cys	Ala	Ile	His	Pro	Ile	Pro	Ala	Ser	Leu	Trp	Arg	Lys	Ala		
227		1040				1045			1050								
228	gtt	tgt	ctc	ccc	agc	ata	ctt	tat	cgc	ctt	cac	tgc	ctt	ttg	act		3204
229	Val	Cys	Leu	Pro	Ser	Ile	Leu	Tyr	Arg	Leu	His	Cys	Leu	Leu	Thr		
230		1055				1060			1065								
231	gca	gag	gag	cta	aga	gcc	cag	act	gcc	agc	gat	gct	ggc	gtg	gga		3249
232	Ala	Glu	Glu	Leu	Arg	Ala	Gln	Thr	Ala	Ser	Asp	Ala	Gly	Val	Gly		
233		1070				1075			1080								
234	gtc	aga	tca	ctt	cct	gcg	gat	ttt	aga	tac	cct	aac	tta	gac	ttc		3294
235	Val	Arg	Ser	Leu	Pro	Ala	Asp	Phe	Arg	Tyr	Pro	Asn	Leu	Asp	Phe		
236		1085				1090			1095								
237	ggg	tgg	aaa	aaa	tct	att	gac	agc	aaa	tct	ttc	atc	tca	att	tct		3339
238	Gly	Trp	Lys	Lys	Ser	Ile	Asp	Ser	Lys	Ser	Phe	Ile	Ser	Ile	Ser		
239		1100				1105			1110								
240	aac	tcc	tct	tca	gct	gaa	aat	gat	aat	tac	tgt	aag	cac	agc	aca		3384
241	Asn	Ser	Ser	Ser	Ala	Glu	Asn	Asp	Asn	Tyr	Cys	Lys	His	Ser	Thr		
242		1115				1120			1125								
243	att	gtc	cct	gaa	aat	gct	gca	cat	caa	ggt	gct	aat	aga	acc	tcc		3429
244	Ile	Val	Pro	Glu	Asn	Ala	Ala	His	Gln	Gly	Ala	Asn	Arg	Thr	Ser		
245		1130				1135			1140								
246	tct	cta	gaa	aat	cat	gac	caa	atg	tct	gtg	aac	tgc	aga	acg	ttg		3474
247	Ser	Leu	Glu	Asn	His	Asp	Gln	Met	Ser	Val	Asn	Cys	Arg	Thr	Leu		
248		1145				1150			1155								
249	ctc	agc	gag	tcc	cct	ggt	aag	ctc	cac	gat	ttt	tca	gca	gat		3519	
250	Leu	Ser	Glu	Ser	Pro	Gly	Lys	Leu	His	Val	Glu	Val	Ser	Ala	Asp		

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